IN THE SPECIFICATION

At page 6, substitute for the first full paragraph:

FIG. 3A. Fragment A and adjacent vector sequences (SEQ ID NO: 1) in the 10d subclone of 772 C_{BE}. This differs from the published 772 C_{BE} sequence (Genbank M25718) in the number of CTT repeats (bp 173-229) and in the presence of A instead of C at bp 116. FIG. 3B. Fragment B and adjacent vector sequences (SEQ ID NO: 2) in the 8a subclone of Lambda 5R. A related sequence on file (Genbank X05913) varied somewhat from the Lambda 5R subclone studied.

Substitute for the paragraph which spans pages 6 and 7:

FIG. 5. Effects of methylation and point mutations in fragment A on DNA-binding. FIG. 5A. Methylation interference assay. "B"-bound DNA recovered from the immunoprecipitate. "C"-equivalent amount of control DNA fragments, not subject to binding reaction. Bound and control DNA samples were cleaved at methylated guanines and equal amounts separated by electrophoresis on a 6% denaturing gel. Dots represent methylation-sensitive sites (open for partial, solid for strong interference); some variation in band intensities occurred between assays, and only the reproducible changes are marked. Right gel shows nucleotides 101-131 of SEQ ID NO: 1 from bottom of gel to top of gel. Left gel shows nucleotides 126-94 of the complementary strand of SEQ ID NO: 1 from bottom of gel to top of gel. At bottom of gel the nucleotides 107-125 of SEQ ID NO: 1 and its complement are shown. FIG. 5B. Binding of "mutant" subfragments of fragment A (Smut1 and 5mut2) to purified baculovirus-produced p53 is compared to that of the normal subfragment 5 sequence. 5mut1 contains a T instead of G at bp 120, and 5mut2 contains Ts in place of Gs at bp 120, 121, and 122.

Substitute for the first full paragraph on page 8 (which was previously amended on March 21, 2005):

Figs. 10A-10D. Definition of a consensus binding site for p53. Figs. 10A and 10B. The p53 binding site of ~~18~~ twenty cloned human genomic DNA fragments (as shown in SEQ ID NO: 4-23), determined by footprinting methods are displayed along the central axis of symmetry which separates the two 10 bp consensus monomers (monomer sequence is shown in SEQ ID NO: 3). Nucleotides in capital letters represent identity of a genomic sequence to the consensus, whereas lower case letters identify disparity with the consensus. Sequences surrounding the consensus or separating the two 10 bp monomers are also shown in lower case. The ten synthetic oligonucleotides (as shown in SEQ ID NO: 24-33) investigated for the ability to be bound by p53 are shown at the bottom of Figs. 10C and 10D. Oligonucleotides No. 6 to 10 (SEQ ID NO: 29-33) were tested after cloning into plasmid vectors. Lower case letters represent vector-derived sequences. Combined nucleotide usage (%) within the two monomers of the consensus binding site is shown in the top portion of Figs. 10C and 10D.